GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:05:57 ; Search time 17398.4 Seconds
(without alignments)
1042.620 Million cell updates/sec

Title: US-09-303-518D-127
Perfect score: 1344
Sequence: 1 atgattaaaatcaaaaaagg.....ccnttgagaaggaaggctga 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	108.6	8.1	349	12	CNS07GYI	AL610380 Anopheles
2	39.2	2.9	540	10	BF260729	BF260729 HVSMEf002
3	39.2	2.9	544	10	BF260723	BF260723 HVSMEf002
4	39.2	2.9	551	10	BF253989	BF253989 HVSMEf000
5	39.2	2.9	574	10	BF265938	BF265938 HV_CEa001
6	39.2	2.9	622	10	BI957371	BI957371 HVSMEn000
7	39.2	2.9	634	10	BI959896	BI959896 HVSMEn002
8	39.2	2.9	636	10	BI959473	BI959473 HVSMEn001
9	39.2	2.9	704	10	BF628632	BF628632 HVSMEb000
10	39.2	2.9	759	10	BF259476	BF259476 HVSMEf001
11	39.2	2.9	764	10	BF616515	BF616515 HVSMEc001
12	39.2	2.9	783	10	BF626740	BF626740 HVSMEb000
13	39.2	2.9	841	10	BF254527	BF254527 HVSMEf000
14	39.2	2.9	847	10	BI957008	BI957008 HVSMEn000
15	39.2	2.9	864	10	BI957786	BI957786 HVSMEn001
16	39.2	2.9	888	9	AW983120	AW983120 HVSMEg000
17	39	2.9	506	9	AI399239	AI399239 NCW10F2T3
18	39	2.9	621	10	BM490565	BM490565 pgp2n.pk0
19	38.2	2.8	455	10	BI956450	BI956450 HVSMEn000
20	37.6	2.8	489	9	AV939450	AV939450 AV939450
21	37.6	2.8	492	10	BE348841	BE348841 ht74g05.x
22	37.6	2.8	575	10	BE551347	BE551347 7b63d11.x
23	37.6	2.8	697	10	BF628426	BF628426 HVSMEb000
24	37.2	2.8	841	10	BG342965	BG342965 HVSMEg000
c 25	37	2.8	430	12	AZ049555	AZ049555 GSSBru013
26	37	2.8	497	12	P947R	AL390645 Leishmani
27	36.8	2.7	893	9	AL523270	AL523270 AL523270
c 28	36.6	2.7	612	12	AQ161443	AQ161443 mgxb0007D
29	36.4	2.7	388	10	BM375129	BM375129 EBem06_SQ
30	36.2	2.7	682	9	AV917449	AV917449 AV917449
c 31	36	2.7	284	9	BE063171	BE063171 QV2-BT027
32	36	2.7	298	9	AA831113	AA831113 oc59a03.s
33	36	2.7	358	10	BF109446	BF109446 7152b06.x
c 34	36	2.7	384	9	AI392198	AI392198 NCSM1D6T3
35	36	2.7	393	9	AI306569	AI306569 qn23e08.x
36	36	2.7	400	9	AI609778	AI609778 tf83b11.x
37	36	2.7	419	9	AA468664	AA468664 ne06c06.s
38	36	2.7	477	9	AI300364	AI300364 qn22e08.x
39	36	2.7	486	9	AI039130	AI039130 ox31a04.s
40	36	2.7	488	9	AI378387	AI378387 tc78e04.x
41	36	2.7	497	9	AI701002	AI701002 we09e08.x
42	36	2.7	526	9	AW006812	AW006812 wt07f12.x
43	36	2.7	544	9	AI743812	AI743812 wg42b09.x
c 44	36	2.7	925	12	CNS0091P	AL053013 Drosophil
c 45	35.8	2.7	932	12	CNS01KFO	AL148277 Anopheles
c 46	35.8	2.7	1013	12	CNS04M5Y	AL297007 Tetraodon
47	35.6	2.6	413	9	AV631377	AV631377 AV631377
48	35.6	2.6	606	12	AQ160470	AQ160470 mgxb0005J
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51	35.4	2.6	421	10	BE423134	BE423134 WHE0061_F
52	35.4	2.6	479	10	BF293599	BF293599 WHE2158_G
53	35.4	2.6	526	10	BG262921	BG262921 WHE0948_G
54	35.4	2.6	561	10	BG262203	BG262203 WHE0873_B
55	35.4	2.6	580	10	BE430910	BE430910 SUN008.D0
56	35.4	2.6	599	10	BF483435	BF483435 WHE1794_H
57	35.4	2.6	617	12	AZ935303	AZ935303 BJ__Ba000
58	35.4	2.6	642	9	AA263267	AA263267 LD06355.5
59	35.4	2.6	702	10	BE414023	BE414023 SCU005.E0
60	35.4	2.6	704	10	BE413893	BE413893 SCU004.B0
61	35.4	2.6	849	10	BE642582	BE642582 Cri2_6_H0
62	35.2	2.6	613	10	BG577607	BG577607 Tm_ad_08D
c 63	35.2	2.6	642	9	AV273615	AV273615 AV273615
c 64	35.2	2.6	684	12	AZ085775	AZ085775 RPCI-23-2
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66	35	2.6	356	10	H83299	H83299 ys89e09.s1
67	35	2.6	429	9	AI816996	AI816996 wj59c01.x
c 68	35	2.6	458	9	AW714071	AW714071 h5f02ne.f
69	35	2.6	620	10	BE425512	BE425512 WHE0317_B
70	35	2.6	802	9	AW448311	AW448311 BRY_541 B
71	35	2.6	826	10	BF624680	BF624680 HVSMEa001
c 72	35	2.6	892	10	BI836975	BI836975 603084506
73	34.8	2.6	275	9	AW574530	AW574530 UI-HF-BK0
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c 75	34.6	2.6	323	9	AI368671	AI368671 qy61h02.x
76	34.6	2.6	376	10	BF293584	BF293584 WHE2158_E
c 77	34.6	2.6	407	9	AW712028	AW712028 f7c01ne.f
78	34.6	2.6	433	9	AW238848	AW238848 xb29f02.y
79	34.6	2.6	497	10	BE378302	BE378302 601236326
80	34.6	2.6	501	10	BE396602	BE396602 601288849
81	34.6	2.6	525	10	BE407307	BE407307 601301064
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83	34.6	2.6	582	10	BM042302	BM042302 603616381
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90	34.6	2.6	659	10	BE254129	BE254129 601113992

91	34.6	2.6	671	10	BE794312	BE794312 601591447
92	34.6	2.6	676	10	BM042451	BM042451 603616281
93	34.6	2.6	683	10	BM006767	BM006767 603615691
94	34.6	2.6	686	10	BG761861	BG761861 602718068
95	34.6	2.6	691	10	BG469125	BG469125 602511078
96	34.6	2.6	721	10	BE299424	BE299424 601118749
97	34.6	2.6	727	10	BE612759	BE612759 601452328
98	34.6	2.6	733	10	BG165939	BG165939 602344259
99	34.6	2.6	762	10	BI161016	BI161016 602865226
100	34.6	2.6	764	10	BG481496	BG481496 602528880

ALIGNMENTS

RESULT 1
CNS07GYI
LOCUS CNS07GYI 349 bp DNA linear GSS 02-OCT-2001
DEFINITION Anopheles gambiae GSS T7 end of clone 23L04 of library NotreDame1 from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION AL610380
VERSION AL610380.1 GI:15916565
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 349)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
REFERENCE 2 (bases 1 to 349)
AUTHORS Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
COMMENT This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.
FEATURES Location/Qualifiers
source 1. .349
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="23L04"
/clone_lib="NotreDame1"
/note="end : T7"
BASE COUNT 72 a 100 c 106 g 71 t
ORIGIN

Query Match 8.1%; Score 108.6; DB 12; Length 349;
Best Local Similarity 59.0%; Pred. No. 1e-19;
Matches 186; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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Db     32 ATGAGTTTGCTGGCCCGCATCCGGCGGGTCTGGTCGGGACGCACATCCATTTCCTTGAGC 91

Qy    689 cggtcggtgcaaacaaaaccgtttggaccatcaattatcaagatgtaattgccatcggac 748
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Db     92 CGGTGAGCCTGACAAAACAGGTCTGGCATCTTAATTATCAGGACGTCATCGCCATCGGTA 151

Qy    749 gtttgtttgcaacaggccgtctgaacaccgagcgcgtgattgctttgggtggttctcaag 808
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Qy    809 tcaacaaaccacgcctcttgcgtaccgttttgggtgcgaaagtatcgcaaattactgcgg 868
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Qy    869 gcgaattggttgacgcagacaaccgcgtgatttccggttcggtattgaacggcgcgatta 928
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Db    272 AAGAAACCAAAGCAGGCGAAAACCGGCTGATTTCCGGTTCGGTCCTCAGTGGCCTGCATG 331

Qy    929 cacaaggcgcgcacg 943
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Db    332 CCGTGCAGGCGCACG 346
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RESULT 2
BF260729
LOCUS BF260729 540 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEf0022M15f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0022M15f, mRNA sequence.
ACCESSION BF260729
VERSION BF260729.2 GI:13120922
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 540)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library
JOURNAL Unpublished (2001)
COMMENT On Nov 16, 2000 this sequence version replaced gi:11189842.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 241
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 530.
FEATURES Location/Qualifiers
source 1. .540
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEf0022M15f"
/clone_lib="Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 111 a 165 c 174 g 90 t
ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 540;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Db    167 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 226

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    227 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 286

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    287 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 346

Qy   1088 agttcacgacagccgt 1103
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Db    347 AGGCCAAGAGCGCCGT 362
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RESULT 3
BF260723
LOCUS BF260723 544 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEf0022M09f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0022M09f, mRNA sequence.
ACCESSION BF260723
VERSION BF260723.2 GI:13120919
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 544)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library
JOURNAL Unpublished (2001)
COMMENT On Nov 16, 2000 this sequence version replaced gi:11189836.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 250
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 512.
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/cultivar="Morex"
/db_xref="taxon:4513"
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/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 110 a 165 c 174 g 92 t 3 others
ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 544;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    167 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 226

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    287 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 346

Qy   1088 agttcacgacagccgt 1103
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Db    347 AGGCCAAGAGCGCCGT 362
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RESULT 4
BF253989
LOCUS BF253989 551 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEf0002L01f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0002L01f, mRNA sequence.
ACCESSION BF253989
VERSION BF253989.2 GI:13116854
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 551)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library
JOURNAL Unpublished (2001)
COMMENT On Nov 16, 2000 this sequence version replaced gi:11183094.
Contact: Wing RA

```
           Clemson University Genomics Institute
           Clemson University
           100 Jordan Hall, Clemson, SC 29634, USA
           Tel: 864 656 7288
           Fax: 864 656 4293
           Email: rwing@clemson.edu
           Total hq bases = 300
           Seq primer: AATTAACCCTCACTAAAGGG
           High quality sequence stop: 540.
FEATURES             Location/Qualifiers
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                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEf0002L01f"
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                     HVcDNA0007 (Etiolated and unstressed)"
                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedling roots were
                     then harvested, total RNA was prepared, poly(A) RNA was
                     purified, one primary unamplified cDNA library was made,
                     and 1 million pfu were in vivo excised to give pBluescript
                     SK(-) cDNA phagemids. These steps were performed in the TJ
                     Close laboratory at the University of California,
                     Riverside (Choi, Close, Fenton). Phagemids were plated and
                     picked at the Clemson University Genomics Institute (CUGI)
                     (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      128 a    151 c    175 g     96 t      1 others
ORIGIN


  Query Match             2.9%;  Score 39.2;  DB 10;  Length 551;
  Best Local Similarity   50.0%;  Pred. No. 4.3;
  Matches   98;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |    ||| ||| ||   |  |   || | | ||||
Db     25 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 84

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  |||  | |||| ||
Db     85 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 144

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||    |     || | | | | | | |  |   ||    |
Db    145 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 204

Qy   1088 agttcacgacagccgt 1103
          ||  || ||  |||||
Db    205 AGGCCAAGAGCGCCGT 220


RESULT   5
BF265938
LOCUS       BF265938                574 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  HV_CEa0013L17f Hordeum vulgare seedling green leaf EST library
            HVcDNA0004 (Blumeria challenged) Hordeum vulgare cDNA clone
            HV_CEa0013L17f, mRNA sequence.
ACCESSION   BF265938
VERSION     BF265938.2  GI:13262431
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 574)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
            Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
            ,D.W., Fenton,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Blumeria infected incompatible (Mla13)
            seedling leaf cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Nov 17, 2000 this sequence version replaced gi:11196932.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 348
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 538.
FEATURES             Location/Qualifiers
     source          1. .574
                     /organism="Hordeum vulgare"
                     /cultivar="CI16155 (Mla13)"
                     /db_xref="taxon:4513"
                     /clone="HV_CEa0013L17f"
                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0004 (Blumeria challenged)"
                     /tissue_type="seedling green leaf"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     C.I. 16155 (Mla13) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate A27 (AvrMla13
                     ) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     cDNA library was made, and 1 million pfu were in vivo
                     excised to give pBluescript SK(-) cDNA phagemids (Choi,
                     Close). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      119 a    177 c    178 g    100 t
ORIGIN


  Query Match             2.9%;  Score 39.2;  DB 10;  Length 574;
  Best Local Similarity   50.0%;  Pred. No. 4.4;
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  Matches   98;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     178 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 237

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     238 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 297

Qy    1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||    |     || | | | | | | |  |  ||    |
Db     298 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 357

Qy    1088 agttcacgacagccgt 1103
           ||  || ||  |||||
Db     358 AGGCCAAGAGCGCCGT 373


RESULT   6
BI957371
LOCUS       BI957371                 622 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0009D13f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0009D13f, mRNA sequence.
ACCESSION   BI957371
VERSION     BI957371.1  GI:16308624
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 318
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 529.
FEATURES             Location/Qualifiers
     source          1. .622
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEn0009D13f"
                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at Washington State University,
                     Pullman, WA in a greenhouse, the rachises were excised and
                     frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
                     lab at the University of California, Riverside total RNA
                     was prepared, poly(A) was purified, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Chin). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
                     sequence has been trimmed to remove vector sequence and
                     contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT       127 a    206 c    183 g    106 t
ORIGIN


  Query Match             2.9%;  Score 39.2;  DB 10;  Length 622;
  Best Local Similarity   50.0%;  Pred. No. 4.6;
  Matches   98;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     185 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 244

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     245 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 304

Qy    1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||    |     || | | | | | | |  |  ||    |
Db     305 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 364

Qy    1088 agttcacgacagccgt 1103
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Db     365 AGGCCAAGAGCGCCGT 380


RESULT   7
BI959896
LOCUS       BI959896                 634 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0022E12f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0022E12f, mRNA sequence.
ACCESSION   BI959896
VERSION     BI959896.1  GI:16311151
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 634)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 465
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 605.
FEATURES             Location/Qualifiers
     source          1. .634
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEn0022E12f"
                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
```

/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 131 a 185 c 205 g 113 t
ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 634;
Best Local Similarity 50.0%; Pred. No. 4.6;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    177 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 236

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  |||  | ||||  ||
Db    237 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 296

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||    |     || | | | | | | |  |   ||    |
Db    297 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 356

Qy   1088 agttcacgacagccgt 1103
           ||  || ||  |||||
Db    357 AGGCCAAGAGCGCCGT 372
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RESULT 8
BI959473
LOCUS BI959473 636 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEn0019N03f Hordeum vulgare rachis EST library HVcDNA0015 (normal) Hordeum vulgare cDNA clone HVSMEn0019N03f, mRNA sequence.
ACCESSION BI959473
VERSION BI959473.1 GI:16310728
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 636)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 585
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 5
High quality sequence stop: 624.
FEATURES Location/Qualifiers
source 1. .636
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEn0019N03f"
/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015 (normal)"
/tissue_type="Rachis"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 132 a 188 c 203 g 113 t
ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 636;
Best Local Similarity 50.0%; Pred. No. 4.6;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    175 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 234

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  |||  | ||||  ||
Db    235 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 294

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||    |     || | | | | | | |  |   ||    |
Db    295 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 354

Qy   1088 agttcacgacagccgt 1103
           ||  || ||  |||||
Db    355 AGGCCAAGAGCGCCGT 370
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RESULT 9
BF628632
LOCUS BF628632 704 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEb0006N12f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMEb0006N12f, mRNA sequence.
ACCESSION BF628632
VERSION BF628632.2 GI:13090280

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KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex drought-stressed seedling shoot cDNA
            library
  JOURNAL   Unpublished (2001)
COMMENT     On Dec 19, 2000 this sequence version replaced gi:11892790.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 580
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .704
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEb0006N12f"
                     /clone_lib="Hordeum vulgare seedling shoot EST library
                     HVcDNA0002 (Dehydration stress)"
                     /tissue_type="Seedling shoot"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedlings were
                     incubated at 90% RH for 24 hr. Shoots were then harvested,
                     total RNA was prepared, poly(A) RNA was purified, one
                     primary unamplified cDNA library was made, 600000 pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids.
                     These steps were performed in the TJ Close laboratory at
                     the University of California, Riverside (Choi, Close,
                     Fenton). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      146 a    206 c    226 g    126 t
ORIGIN


  Query Match             2.9%;  Score 39.2;  DB 10;  Length 704;
  Best Local Similarity   50.0%;  Pred. No. 4.9;
  Matches   98;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     164 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 223

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     224 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 283

Qy    1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||     |     || | | | | | | | |   ||    |
Db     284 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 343

Qy    1088 agttcacgacagccgt 1103
           ||  || ||  |||||
Db     344 AGGCCAAGAGCGCCGT 359


RESULT  10
BF259476
LOCUS       BF259476                759 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEf0019D11f Hordeum vulgare seedling root EST library HVcDNA0007
            (Etiolated and unstressed) Hordeum vulgare cDNA clone
            HVSMEf0019D11f, mRNA sequence.
ACCESSION   BF259476
VERSION     BF259476.2  GI:13119939
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex unstressed seedling root cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Nov 16, 2000 this sequence version replaced gi:11188505.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 469
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEf0019D11f"
                     /clone_lib="Hordeum vulgare seedling root EST library
                     HVcDNA0007 (Etiolated and unstressed)"
                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedling roots were
                     then harvested, total RNA was prepared, poly(A) RNA was
                     purified, one primary unamplified cDNA library was made,
                     and 1 million pfu were in vivo excised to give pBluescript
                     SK(-) cDNA phagemids. These steps were performed in the TJ
                     Close laboratory at the University of California,
                     Riverside (Choi, Close, Fenton). Phagemids were plated and
                     picked at the Clemson University Genomics Institute (CUGI)
                     (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
```

preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 190 a 210 c 230 g 127 t 2 others
ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 759;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
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Db     32 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 91

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db     92 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 151

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    152 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 211

Qy   1088 agttcacgacagccgt 1103
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Db    212 AGGCCAAGAGCGCCGT 227
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RESULT 11
BF616515
LOCUS BF616515 764 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEc0010E03f Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEc0010E03f, mRNA sequence.
ACCESSION BF616515
VERSION BF616515.2 GI:13108021
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 764)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library
JOURNAL Unpublished (2001)
COMMENT On Dec 18, 2000 this sequence version replaced gi:11880249.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 395
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 623.
FEATURES Location/Qualifiers
source 1. .764
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEc0010E03f"
/clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 177 a 217 c 243 g 127 t
ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 764;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
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Db    167 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 226

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    227 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 286

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||    |     || | | | | | | |   |   ||    |
Db    287 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 346

Qy   1088 agttcacgacagccgt 1103
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Db    347 AGGCCAAGAGCGCCGT 362
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RESULT 12
BF626740
LOCUS BF626740 783 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEb0001D17f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMEb0001D17f, mRNA sequence.
ACCESSION BF626740
VERSION BF626740.2 GI:13088174
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 783)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA library
JOURNAL Unpublished (2001)

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COMMENT     On Dec 19, 2000 this sequence version replaced gi:11890904.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 476
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 698.
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEb0001D17f"
                     /clone_lib="Hordeum vulgare seedling shoot EST library
                     HVcDNA0002 (Dehydration stress)"
                     /tissue_type="Seedling shoot"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedlings were
                     incubated at 90% RH for 24 hr. Shoots were then harvested,
                     total RNA was prepared, poly(A) RNA was purified, one
                     primary unamplified cDNA library was made, 600000 pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids.
                     These steps were performed in the TJ Close laboratory at
                     the University of California, Riverside (Choi, Close,
                     Fenton). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      177 a    220 c    252 g    134 t
ORIGIN
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  Query Match             2.9%;  Score 39.2;  DB 10;  Length 783;
  Best Local Similarity   50.0%;  Pred. No. 5.1;
  Matches   98;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||     |      ||| ||| ||   |  |     || | | ||||
Db     178 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 237

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db     238 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 297

Qy    1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
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Db     298 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 357

Qy    1088 agttcacgacagccgt 1103
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Db     358 AGGCCAAGAGCGCCGT 373
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RESULT 13

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BF254527
LOCUS       BF254527                841 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEf0004E12f Hordeum vulgare seedling root EST library HVcDNA0007
            (Etiolated and unstressed) Hordeum vulgare cDNA clone
            HVSMEf0004E12f, mRNA sequence.
ACCESSION   BF254527
VERSION     BF254527.2  GI:13117183
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 841)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex unstressed seedling root cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Nov 16, 2000 this sequence version replaced gi:11183632.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 416
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 580.
FEATURES             Location/Qualifiers
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                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
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                     /clone_lib="Hordeum vulgare seedling root EST library
                     HVcDNA0007 (Etiolated and unstressed)"
                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedling roots were
                     then harvested, total RNA was prepared, poly(A) RNA was
                     purified, one primary unamplified cDNA library was made,
                     and 1 million pfu were in vivo excised to give pBluescript
                     SK(-) cDNA phagemids. These steps were performed in the TJ
                     Close laboratory at the University of California,
                     Riverside (Choi, Close, Fenton). Phagemids were plated and
                     picked at the Clemson University Genomics Institute (CUGI)
                     (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      192 a    219 c    298 g    132 t
ORIGIN
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  Query Match             2.9%;  Score 39.2;  DB 10;  Length 841;
  Best Local Similarity   50.0%;  Pred. No. 5.3;
  Matches   98;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;
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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    180 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 239

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    240 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 299

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    300 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 359

Qy   1088 agttcacgacagccgt 1103
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Db    360 AGGCCAAGAGCGCCGT 375


RESULT 14
BI957008
LOCUS       BI957008                847 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0006O06f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0006O06f, mRNA sequence.
ACCESSION   BI957008
VERSION     BI957008.1  GI:16308261
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 847)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 592
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
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                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
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                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at Washington State University,
                     Pullman, WA in a greenhouse, the rachises were excised and
                     frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
                     lab at the University of California, Riverside total RNA
                     was prepared, poly(A) was purified, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Chin). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
                     sequence has been trimmed to remove vector sequence and
                     contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      183 a    249 c    258 g    157 t
ORIGIN


  Query Match             2.9%;  Score 39.2;  DB 10;  Length 847;
  Best Local Similarity   50.0%;  Pred. No. 5.3;
  Matches   98;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    180 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 239

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    240 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 299

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||     |     || | | | | | | |  |   ||    |
Db    300 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 359

Qy   1088 agttcacgacagccgt 1103
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Db    360 AGGCCAAGAGCGCCGT 375


RESULT 15
BI957786
LOCUS       BI957786                864 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0011F07f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0011F07f, mRNA sequence.
ACCESSION   BI957786
VERSION     BI957786.1  GI:16309053
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 458
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
     source          1. .864
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEn0011F07f"
                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
                     /lab_host="TJC121"
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 188 a 221 c 324 g 131 t
ORIGIN

Query Match 2.9%; Score 39.2; DB 10; Length 864;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    114 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 173

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db    174 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 233

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||    |     || | | | | | | |  |   ||    |
Db    234 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 293

Qy   1088 agttcacgacagccgt 1103
          ||  || ||  |||||
Db    294 AGGCCAAGAGCGCCGT 309
```

RESULT 16
AW983120
LOCUS AW983120 888 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEg0008D22f Hordeum vulgare pre-anthesis spike EST library HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone HVSMEg0008D22f, mRNA sequence.
ACCESSION AW983120
VERSION AW983120.3 GI:16317593
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 888)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Close,S.J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex pre-anthesis spike cDNA library
JOURNAL Unpublished (2001)
COMMENT On Jun 2, 2000 this sequence version replaced gi:13153638.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 448
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 592.
FEATURES Location/Qualifiers
source 1. .888
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEg0008D22f"
/clone_lib="Hordeum vulgare pre-anthesis spike EST library HVcDNA0008 (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spike with awns trimmed were collected at white, green and yellow anther stages (Fenton). Total RNA was prepared from each pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close lab (Choi) at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch , Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 195 a 248 c 283 g 162 t
ORIGIN

Query Match 2.9%; Score 39.2; DB 9; Length 888;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

```
Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    166 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 225

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db    226 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 285

Qy   1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||    |     || | | | | | | |  |   ||    |
Db    286 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 345

Qy   1088 agttcacgacagccgt 1103
          ||  || ||  |||||
Db    346 AGGCCAAGAGCGCCGT 361
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RESULT 17
AI399239
LOCUS AI399239 506 bp mRNA linear EST 08-FEB-1999
DEFINITION NCW10F2T3 Westergaards Neurospora crassa cDNA clone W10F2 5', mRNA sequence.
ACCESSION AI399239

```
VERSION     AI399239.1  GI:4242324
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
            Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
            Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R.
            , Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R.,
            Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig
            ,D.O.
  TITLE     Expressed sequences from conidial, mycelial, and sexual stages of
            Neurospora crassa
  JOURNAL   Fungal Genet. Biol. 21, 348-363 (1997)
  MEDLINE   97435549
COMMENT     Contact: Natvig,D.O./Nelson,M.A.
            Department of Biology
            University of New Mexico
            Castetter Hall, Albuquerque, NM 87131, USA
            Tel: 505 277 3411
            Fax: 505 277 0304
            Email: ngp@biology.unm.edu.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Neurospora crassa"
                     /strain="74-OR23-IV A (FGSC 2489)"
                     /db_xref="taxon:5141"
                     /clone="W10F2"
                     /clone_lib="Westergaards"
                     /sex="Mating type A"
                     /tissue_type="Unfertilized sexual tissue"
                     /dev_stage="Unfertilized sexual stage"
                     /lab_host="E. coli"
                     /note="Vector: pBlueScript SK (-); Site_1: EcoRI; Site_2:
                     XhoI; Westergaard's medium (Nitrogen limiting). Floating
                     mycelial mats grown at 25C for 36 hours. cDNA
                     directionally cloned into pBluescript SK(-) using the
                     Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
BASE COUNT      105 a    136 c    132 g    129 t      4 others
ORIGIN


  Query Match             2.9%;  Score 39;  DB 9;  Length 506;
  Best Local Similarity   48.7%;  Pred. No. 4.7;
  Matches   96;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy     100 gaagaatatgccggtatgcgcccctngatgaaagtcaaggaaggcgatgccgtcaaaaaa 159
           || ||   |||||   |  ||  |  | |||    | |||| ||  | || | |   ||
Db      27 GAGGACATTGCCGCCTTCAGCTTCCAGTTGATTCCCCAGGACGGTAAGGCTGCCGTCAAG 86

Qy     160 ggccaagtgctgtttgaagacaaaaagnatccgggcgtggtgtttaccgcgccngtttca 219
           || ||  |||        || || |     || |||     ||   |  |  | |  ||
Db      87 GGGCAGTTGCGCAAGCGGGAGAACANCGTCCCTGGCCCATCGTCNTCGTCCGCCGCATCG 146

Qy     220 ggcaaaatcgccgccatccatcgcggcgaaaagcgcgtacttcagtcggtcgtgattgcc 279
           |  |     | ||| |||||| ||| ||  ||  ||       ||  |  |    ||||
Db     147 GCTAGCGGGGGCGCTATCCATGGCGCCGTTAACGGCACCGGAAAGATGCACCACTTTGCT 206

Qy     280 gttgaaggcaacgacga 296
           ||| || |||   || |
Db     207 GTTAAAAGCAGAAACNA 223


RESULT  18
BM490565
LOCUS       BM490565                621 bp    mRNA    linear   EST 07-FEB-2002
DEFINITION  pgp2n.pk003.m9 Normalized Chicken Pituitary/Hypothalamus/Pineal
            Library (pgp2n) Gallus gallus cDNA clone pgp2n.pk003.m9 5' similar
            to ref|XP_051773.2 (XM_051773) deltex (Drosophila) homolog 1 [Homo
            sapiens], mRNA sequence.
ACCESSION   BM490565
VERSION     BM490565.1  GI:18611496
KEYWORDS    EST.
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Porter,T.E. and Cogburn,L.A.
  TITLE     ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
            library, USDA/IFAFS Animal Genome Project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Gallus gallus"
                     /strain="Commercial broiler chickens"
                     /db_xref="taxon:9031"
                     /clone="pgp2n.pk003.m9"
                     /clone_lib="Normalized Chicken
                     Pituitary/Hypothalamus/Pineal Library (pgp2n)"
                     /sex="Male and Female"
                     /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
                     /dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9
                     weeks)"
                     /lab_host="E. coli EMDH10B"
                     /note="Vector: pCMVSPORT6; Library made from equivalent
                     pools of total RNA isolated from each tissue at different
                     ages. Single pass sequencing from 5'-end"
BASE COUNT      116 a    217 c    193 g     95 t
ORIGIN


  Query Match             2.9%;  Score 39;  DB 10;  Length 621;
  Best Local Similarity   51.4%;  Pred. No. 5.2;
  Matches   90;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy     956 gctaccacaatcagatttccgttatcgaagaaggccgcagcaaagagctgttcggctggg 1015
           || ||||||   |||      | |  || || | |||  |||  | | || | |||  ||
Db      65 GCCACCACATCGAGAACGTGCTGAAGGAGGATGCCCGTGGCAGCGTGGTGCTGGGCCAGG 124

Qy    1016 ttgcgccgcagccggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaa 1075
           | |    ||||| ||     |||  ||||    |    | || |   ||| |||| | |
Db     125 TGGACGTGCAGCTGGCACCCTACATCATCGACCTGCAGTCCATGCACCAGTTCCGGCAGG 184

Qy    1076 acaaactcttcaagttcacgacagccgtcaacggtggcgaccgcgccatggtgcc 1130
           |||    |  || |  | ||     |   |||     ||||| | ||  ||  ||
Db     185 ACACGGGCACCATGCGCCCGGTGCGCAGGAACTTCTACGACCCCTCCTCGGCACC 239


RESULT  19
BI956450
LOCUS       BI956450                455 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0003G23f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0003G23f, mRNA sequence.
ACCESSION   BI956450
VERSION     BI956450.1  GI:16307703
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
```

```
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 327
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 453.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEn0003G23f"
                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at Washington State University,
                     Pullman, WA in a greenhouse, the rachises were excised and
                     frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
                     lab at the University of California, Riverside total RNA
                     was prepared, poly(A) was purified, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Chin). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
                     sequence has been trimmed to remove vector sequence and
                     contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT       83 a    150 c    150 g     70 t      2 others
ORIGIN
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  Query Match             2.8%;  Score 38.2;  DB 10;  Length 455;
  Best Local Similarity   49.5%;  Pred. No. 7.6;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     185 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 244

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     245 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 304

Qy    1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||          || | | | | | | |  |   ||    |
Db     305 TGAGCTCGTACGCCGGACGGCCGCANGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 364

Qy    1088 agttcacgacagccgt 1103
           ||  || ||  |||||
Db     365 AGGCCAAGAGCGCCGT 380


RESULT  20
AV939450
LOCUS       AV939450                489 bp    mRNA    linear   EST 18-JAN-2002
```

```
DEFINITION  AV939450 K. Sato unpublished cDNA library, strain H602 adult,
            heading stage top three leaves Hordeum vulgare subsp. spontaneum
            cDNA clone bah22i02 5', mRNA sequence.
ACCESSION   AV939450
VERSION     AV939450.1  GI:18235247
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
  ORGANISM  Hordeum vulgare subsp. spontaneum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .489
                     /organism="Hordeum vulgare subsp. spontaneum"
                     /strain="H602"
                     /db_xref="taxon:77009"
                     /clone="bah22i02"
                     /clone_lib="K. Sato unpublished cDNA library, strain H602
                     adult, heading stage top three leaves"
                     /tissue_type="top three leaves"
                     /dev_stage="adult, heading stage"
BASE COUNT       95 a    155 c    162 g     77 t
ORIGIN
```

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  Query Match             2.8%;  Score 37.6;  DB 9;  Length 489;
  Best Local Similarity   49.5%;  Pred. No. 12;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     172 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 231

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     232 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 291

Qy    1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||     |  || | | | | | | |  |   ||    |
Db     292 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 351

Qy    1088 agttcacgacagccgt 1103
           ||  || ||  |||||
Db     352 AGGCTAAGAGCGCCGT 367


RESULT  21
BE348841
LOCUS       BE348841                492 bp    mRNA    linear   EST 18-JUL-2000
DEFINITION  ht74g05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3152504 3'
            similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN C1B1.02C
            IN CHROMOSOME I. ;contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION   BE348841
VERSION     BE348841.1  GI:9260694
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 492)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
```

```
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 480.
FEATURES             Location/Qualifiers
     source          1. .492
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3152504"
                     /clone_lib="NCI_CGAP_Lu24"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
BASE COUNT       97 a    158 c    141 g     96 t
ORIGIN


  Query Match             2.8%;  Score 37.6;  DB 10;  Length 492;
  Best Local Similarity   59.3%;  Pred. No. 12;
  Matches   64;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||| | |
Db     201 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 260

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||| |||   || |||  ||  || ||
Db     261 CGCCCAGTGCCTGCATTGGAACGGCCGGAAGAAGCAAGCCCACTTCGA 308


RESULT  22
BE551347
LOCUS       BE551347                575 bp    mRNA    linear   EST 10-AUG-2000
DEFINITION  7b63d11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3232917 3'
            similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN C1B1.02C
            IN CHROMOSOME I. ;contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION   BE551347
VERSION     BE551347.1  GI:9793039
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 575)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .575
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3232917"
                     /clone_lib="NCI_CGAP_Lu24"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
BASE COUNT      115 a    176 c    162 g    122 t
ORIGIN


  Query Match             2.8%;  Score 37.6;  DB 10;  Length 575;
  Best Local Similarity   59.3%;  Pred. No. 12;
  Matches   64;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||| | |
Db     220 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 279

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||| |||   || |||  ||  || ||
Db     280 CGCCCAGTGCCTGCATTGGAACGGCCGGAAGAAGCAAGCCCACTTCGA 327


RESULT  23
BF628426
LOCUS       BF628426                697 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEb0006A02f Hordeum vulgare seedling shoot EST library
            HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone
            HVSMEb0006A02f, mRNA sequence.
ACCESSION   BF628426
VERSION     BF628426.2  GI:13090049
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex drought-stressed seedling shoot cDNA
            library
  JOURNAL   Unpublished (2001)
COMMENT     On Dec 19, 2000 this sequence version replaced gi:11892584.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 340
            Seq primer: AATTAACCCTCACTAAAGGG
```

```
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .697
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEb0006A02f"
                     /clone_lib="Hordeum vulgare seedling shoot EST library
                     HVcDNA0002 (Dehydration stress)"
                     /tissue_type="Seedling shoot"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedlings were
                     incubated at 90% RH for 24 hr. Shoots were then harvested,
                     total RNA was prepared, poly(A) RNA was purified, one
                     primary unamplified cDNA library was made, 600000 pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids.
                     These steps were performed in the TJ Close laboratory at
                     the University of California, Riverside (Choi, Close,
                     Fenton). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT       144 a    206 c    220 g    126 t      1 others
ORIGIN
```

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  Query Match             2.8%;  Score 37.6;  DB 10;  Length 697;
  Best Local Similarity   49.5%;  Pred. No. 14;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     169 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 228

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     229 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 288

Qy    1028 cggacaaatactccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||    |     || | | | | | | |   |   ||    |
Db     289 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 348

Qy    1088 agttcacgacagccgt 1103
           ||  ||  |  |||||
Db     349 AGGCCAAAAGCGCCGT 364
```

```
RESULT  24
BG342965
LOCUS       BG342965                841 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEg0001H23f Hordeum vulgare pre-anthesis spike EST library
            HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone
            HVSMEg0001H23f, mRNA sequence.
ACCESSION   BG342965
VERSION     BG342965.1  GI:13155294
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 841)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex pre-anthesis spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 335
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .841
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEg0001H23f"
                     /clone_lib="Hordeum vulgare pre-anthesis spike EST library
                     HVcDNA0008 (white to yellow anther)"
                     /tissue_type="pre-anthesis spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spike with awns trimmed were collected at white, green and
                     yellow anther stages (Fenton). Total RNA was prepared from
                     each pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     primary unamplified cDNA library was made, and 1 million
                     pfu were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids. These steps were performed in the TJ Close lab
                     (Choi) at the University of California, Riverside.
                     Phagemids were plated and picked at the Clemson University
                     Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins
                     and Wing) Plasmid DNA preparations, DNA sequencing and
                     sequence analysis were performed at CUGI (Wing, Yu, Frisch
                     , Henry, Simmons, Oates, Rambo, Main). The sequence has
                     been trimmed to remove vector sequence and contains a
                     minimum of 100 bases of phred value 20 or above. For more
                     details on library preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT       209 a    233 c    248 g    151 t
ORIGIN
```

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  Query Match             2.8%;  Score 37.2;  DB 10;  Length 841;
  Best Local Similarity   50.0%;  Pred. No. 19;
  Matches   93;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

Qy     918 cggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatcagatttccgt 977
           || |||    |     ||| ||| ||   |  |    || | | ||||  ||||     |
Db       9 CGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGAAGATGGAGCT 68

Qy     978 tatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagccggacaaata 1037
           |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  || |  |   ||
Db      69 CGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGCTGAGCTCGTA 128

Qy    1038 ctccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttcaagttcacgac 1097
           | ||     ||    |     || | | | | | | |   ||    ||| || ||
```

```
Db    129 CGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGAAGGCCAAGAG 188

Qy   1098 agccgt 1103
          ||||||
Db    189 CGCCGT 194


RESULT  25
AZ049555/c
LOCUS       AZ049555                430 bp    DNA     linear   GSS 06-MAR-2001
DEFINITION  GSSBru01308 Sheared genomic library Brucella melitensis biovar
            Abortus genomic clone M26, DNA sequence.
ACCESSION   AZ049555
VERSION     AZ049555.1  GI:7273470
KEYWORDS    GSS.
SOURCE      Brucella melitensis biovar Abortus.
  ORGANISM  Brucella melitensis biovar Abortus
            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
            Brucellaceae; Brucella.
REFERENCE   1  (bases 1 to 430)
  AUTHORS   Sanchez,D.O., Zandomeni,R.O., Cravero,S., Verdun,R.E., Pierrou,E.,
            Faccio,P., Diaz,G., Lanzavecchia,S., Aguero,F., Frasch,A.C.C.,
            Andersson,S.G.E., Rosetti,O.L., Grau,O. and Ugalde,R.A.
  TITLE     Gene discovery through genomic sequencing of Brucella abortus
  JOURNAL   Infect. Immun. 69 (2), 865-868 (2001)
COMMENT     Contact: Zandomeni, R.
            Centro de Investigacion en Ciencias Agropecuarias (CICA)
            Instituto Nacional de Tecnologia Agropecuaria (INTA) C.C. 25 (1712)
            Castelar. Buenos Aires, Argentina
            Tel: 5411-4621-3316/1683
            Fax: 5411-4481-1316
            Email: zandomeni@inta.gov.ar
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .430
                     /organism="Brucella melitensis biovar Abortus"
                     /strain="S-2308"
                     /db_xref="taxon:235"
                     /clone="M26"
                     /clone_lib="Sheared genomic library"
                     /note="Vector: pBluescript SK(-) (STRATAGENE); Genomic DNA
                     was mechanically sheared, blunt ended, and
                     size-fractionated by agarose gel electrophoresis.
                     Fragments between 1.5-3 Kb were recovered and ligated to
                     the EcoRV site of the pBluescript SK (-) vector."
BASE COUNT       83 a    124 c    127 g     91 t      5 others
ORIGIN


  Query Match             2.8%;  Score 37;  DB 12;  Length 430;
  Best Local Similarity   51.3%;  Pred. No. 16;
  Matches   79;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy    442 gccatcttcgtcaatgcgatggacaccaatccgctngcggcagaccctgtggttgtgatc 501
          |||||  | | | || |    |||||      | | |||| ||     | ||  |   |
Db    221 GCCATGCTGGCCGATCCCGCCGACACGCGGAAGGTGGCGGAAGTGGGAGAGGTGATCGGC 162

Qy    502 aaagaagccgncgangatttcagacgangtntgctggtattgagccgtttgaccgagcgt 561
            ||  ||| ||   ||||||| |||    |   |     |  | |||  |    | |
Db    161 TTTGATTCCGCCGCGAATTTCAGTCGAGCCTTCACGCATCAGTTCGGTTATAGTCCGAGC 102

Qy    562 aaaatccatgtgtgtaaggcagctggcgcagacg 595
          || ||||    |   | |||| ||||||||  ||
Db    101 AATATCCGCAAGCAAACGGCAACTGGCGCACCCG 68


RESULT  26
P947R
LOCUS       P947R                   497 bp    DNA     linear   GSS 25-JUL-2000
DEFINITION  Leishmania major Friedlin PAC P947 right end-sequence, genomic
            survey sequence.
ACCESSION   AL390645
VERSION     AL390645.1  GI:9501621
KEYWORDS    GSS.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Leishmania.
REFERENCE   1  (bases 1 to 497)
  AUTHORS   Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and
            Smith,D.F.
  TITLE     A physical map of the Leishmania major Friedlin genome
  JOURNAL   Genome Res. 8 (2), 135-145 (1998)
  MEDLINE   98146435
REFERENCE   2  (bases 1 to 497)
  AUTHORS   Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and
            Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            alicat@sanger.ac.uk
COMMENT     see http://www.ebi.ac.uk/parasites/leish.html
            Details of Leishmania sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/L_major/
            The primer sequence can be obtained from alicat@sanger.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .497
                     /organism="Leishmania major"
                     /strain="Friedlin"
                     /db_xref="taxon:5664"
                     /clone="PAC P947"
BASE COUNT       74 a    172 c    145 g    104 t      2 others
ORIGIN


  Query Match             2.8%;  Score 37;  DB 12;  Length 497;
  Best Local Similarity   58.7%;  Pred. No. 17;
  Matches   64;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy   1172 ctaccctgcttttgcgcgatttaatcgtcggcgataccgacagcgcgcaagcattgggtt 1231
          | || |||||   || ||  ||   || |||||  |||| |    |||  || | | |
Db    231 CGACGCTGCTGCCGCACGCGTTGCGCGCCGGCGCCACCGTCGCGCCGCCGGCCTAGCGCC 290

Qy   1232 gcttggaattggacgaagaagacctcgctttgtgcagcttcgtctgccc 1280
          ||  | ||  | |||||      ||||| | ||   || |||||| |||
Db    291 GCCAGCAACAGAACGAACCCCGTCTCGCATCGTCATGCGTCGTCTTCCC 339


RESULT  27
AL523270
LOCUS       AL523270                893 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL523270 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC001YH12 5
            prime, mRNA sequence.
ACCESSION   AL523270
VERSION     AL523270.1  GI:12786763
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 893)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DC001YH12"
                     /clone_lib="LTI_NFL003_NBC3"
                     /sex="male"
```

/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen.9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 168 a 282 c 285 g 153 t 5 others
ORIGIN

Query Match 2.7%; Score 36.8; DB 9; Length 893;
Best Local Similarity 54.0%; Pred. No. 26;
Matches 68; Conservative 2; Mismatches 56; Indels 0; Gaps 0;

```
Qy   1215 cgcgcaagcattgggttgcttggaattggacgaagaagacctcgctttgtgcagcttcgt 1274
          || |   |||   |   ||:    |  || ||  || ||    || |  :|| || |
Db    258 CGGGGCTGCAACCGCCAGCKCCTCAGGGGCCGCCGAGGATGGGGCCTGCKGCTGCCTGCC 317

Qy   1275 ctgcccgggcaaatacgaatanggcccgctgttgcgtaaggtgctggaaaccnttgagaa 1334
          |  |||||||| || |||  |  |||  | |  | | |||| ||||    || || |||
Db    318 CAACCCGGGCACATTCGAGGAGTGCCACCGGAAGTGCAAGGAGCTGTTTCCCATTCAGAT 377

Qy   1335 ggaagg 1340
          ||| ||
Db    378 GGAGGG 383
```

RESULT 28
AQ161443/c
LOCUS AQ161443 612 bp DNA linear GSS 09-SEP-1998
DEFINITION mgxb0007D20r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0007D20r, DNA sequence.
ACCESSION AQ161443
VERSION AQ161443.1 GI:3557844
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 612)
AUTHORS Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 258.
FEATURES Location/Qualifiers
source 1. .612
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0007D20r"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
BASE COUNT 118 a 233 c 124 g 137 t
ORIGIN

Query Match 2.7%; Score 36.6; DB 12; Length 612;
Best Local Similarity 44.8%; Pred. No. 25;
Matches 120; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

```
Qy    138 ggaaggcgatgccgtcaaaaaaggccaagtgctgtttgaagacaaaaagnatccgggcgt 197
          ||  ||| ||| |||   | | || |  ||  |  |||||  |       |  ||| |
Db    589 GGTGGGCAATGTCGTTGTACACGGTCTGGTAGTCCTTGAACTCGGGCTTGGTGAGGGTGG 530

Qy    198 ggtgtttaccgcgccngtttcaggcaaaatcgccgccatccatcgcggcgaaaagcgcgt 257
          |     |||| |  | | |  |     || || | ||| |    ||||||  ||| ||
Db    529 CGGCGCCACCGTTCTGGGTGTACCAGTAACCGGCACCAGCAGCAGCGGCGGCAAGGGCAC 470

Qy    258 acttcagtcggtcgtgattgccgttgaaggcaacgacgaaatcgagttcgaacgctacgc 317
            |  | | || | |||       ||||   | ||   |||       |||    |
Db    469 CGGCAATCCAGCCGAGGTTGGACGACGAGGCCTTGGCGGGCTCGGACGAAGACGAGTAGA 410

Qy    318 gcccgaagcgttggcaaacttaagcggcgangaantnngnngcaatctgatccaatccgg 377
            | |  ||   |         ||||||| |       |  |||  | |  | ||  |||
Db    409 AGCGGCGGCCAGCGATGGTGCGGGCGGCGAGGCCGCGTGATGCAGCCGGGGCGAACGCGG 350

Qy    378 tttgtggactgcgctgcgtanccgtccg 405
          |  | |  |||    | |   | | |||
Db    349 TGCGGGTGCTGGCGCGGGACGCAGCCCG 322
```

RESULT 29
BM375129
LOCUS BM375129 388 bp mRNA linear EST 10-JAN-2002
DEFINITION EBem06_SQ002_H03_R IGF Barley EBem06 library Hordeum vulgare cDNA clone EBem06_SQ002_H03 5', mRNA sequence.
ACCESSION BM375129
VERSION BM375129.1 GI:18118519
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 388)
AUTHORS Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE Development of Barley Transcriptome Resources
JOURNAL Unpublished (2001)
COMMENT Contact: Waugh R
Unit of Genomics
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
FEATURES Location/Qualifiers
source 1. .388
/organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
/clone="EBem06_SQ002_H03"
/clone_lib="IGF Barley EBem06 library"
/tissue_type="Embryo"
/dev_stage="21 days post anthesis"

```
                     /lab_host="DH10B"
                     /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
                     Non-normalised library, directionally cloned into pSPORT1.
                     Derived from embryos dissected from developing grains (21
                     days post anthesis) in glasshouse grown barley plants.
                     Developed as part of the barley transcriptome resources of
                     BBSRC/SEERAD funded cereal IGF (Investigating Gene
                     Function) project."
BASE COUNT       65 a    139 c    122 g     62 t
ORIGIN


  Query Match             2.7%;  Score 36.4;  DB 10;  Length 388;
  Best Local Similarity   52.8%;  Pred. No. 22;
  Matches   76;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy    178 gacaaaaagnatccgggcgtggtgtttaccgcgccngtttcaggcaaaatcgccgccatc 237
          | ||  |||   |||    || |||   ||   || ||    |||||  || ||| | ||
Db    166 GTCACCAAGGGCCCGCTGCTGCTGTCGTCCAACCCCGTCCACGGCAAGGTCCCCGTCCTC 225

Qy    238 catcgcggcgaaaagcgcgtacttcagtcggtcgtgattgccgttgaaggcaacgacgaa 297
          |    || ||  |||| ||||    ||||  |||| ||   ||       | |||| |
Db    226 CTCGTCGACGGCAAGCCCGTATGCGAGTCCCTCGTCATCCTCGAGTTCATCGACGAGGCG 285

Qy    298 atcgagttcgaacgctacgcgccc 321
            ||  |  ||   || |  ||| |
Db    286 TTCCCGGGCGCCGGCGAGCCGCTC 309


RESULT  30
AV917449
LOCUS       AV917449                682 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  AV917449 K. Sato unpublished cDNA library, cv. Haruna Nijo
            germination shoots Hordeum vulgare subsp. vulgare cDNA clone
            bags18p10 5', mRNA sequence.
ACCESSION   AV917449
VERSION     AV917449.1  GI:18213226
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 682)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .682
                     /organism="Hordeum vulgare subsp. vulgare"
                     /cultivar="Haruna Nijo"
                     /db_xref="taxon:112509"
                     /clone="bags18p10"
                     /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
                     Nijo germination shoots"
                     /tissue_type="shoots"
                     /dev_stage="germination"
BASE COUNT      170 a    187 c    204 g    120 t      1 others
ORIGIN


  Query Match             2.7%;  Score 36.2;  DB 9;  Length 682;
  Best Local Similarity   49.5%;  Pred. No. 34;
  Matches   92;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;

Qy    918 cggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatcagatttccgt 977
          || |||    |     ||| ||| ||   |  |    || | | ||||  ||||     |
Db     16 CGACGCCGGNAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGAAGATGGAGCT 75

Qy    978 tatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagccggacaaata 1037
            |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  || |  |   ||
Db     76 CGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGCTGAGCTCGTA 135

Qy   1038 ctccatcacgcgtacgaccctcggccatttcctgaaaaacaaactcttcaagttcacgac 1097
           | ||     ||     |      || | | | | | | |  |   ||    |||   | ||
Db    136 CGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGAAGGCTAAGAG 195

Qy   1098 agccgt 1103
            |||||
Db    196 CGCCGT 201


RESULT  31
BE063171/c
LOCUS       BE063171                284 bp    mRNA    linear   EST 09-JUN-2000
DEFINITION  QV2-BT0271-140200-043-b08 BT0271 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE063171
VERSION     BE063171.1  GI:8407821
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 284)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV2-BT0271-140
            200-043-b08&t3=2000-02-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 284.
FEATURES             Location/Qualifiers
     source          1. .284
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT0271"
                     /dev_stage="Adult"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       45 a     91 c     78 g     70 t
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 284;
  Best Local Similarity   58.3%;  Pred. No. 25;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;
```

```
Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||||| | |
Db     162 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 103

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     102 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 55


RESULT  32
AA831113
LOCUS       AA831113                298 bp    mRNA    linear   EST 07-APR-1998
DEFINITION  oc59a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1353964 3'
            similar to SW:YEF1_YEAST P32622 HYPOTHETICAL 55.9 KD PROTEIN IN
            GDA1-UTR2 INTERGENIC REGION. ;contains element TAR1 repetitive
            element ;, mRNA sequence.
ACCESSION   AA831113
VERSION     AA831113.1  GI:2904212
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 298)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 830   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 277.
FEATURES             Location/Qualifiers
     source          1. .298
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1353964"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       69 a    84 c    93 g    52 t
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 298;
  Best Local Similarity   58.3%;  Pred. No. 26;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||||| | |
Db     146 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 205

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     206 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 253


RESULT  33
BF109446
LOCUS       BF109446                358 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  7152b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:3525058 3' similar to TR:Q9V6R5 Q9V6R5 CG6152 PROTEIN. [1]
            ;contains element MER22 repetitive element ;, mRNA sequence.
ACCESSION   BF109446
VERSION     BF109446.1  GI:10939136
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 329.
FEATURES             Location/Qualifiers
     source          1. .358
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3525058"
                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NbHSF pool 1:
                     309384-310919, 323208-325895 Soares Nb2HP pool 1:
                     145032-147335, 147720-148103, 148872-149255, 15002 -
                     150407, 151176-152327 Soares Nb2HF8-9W pool 1:
                     758280-760583, 772104-774407 Soares NbHPA pool 1:
                     304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                     pool 1:  723720-726407, 739080-740999 Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
BASE COUNT       77 a    114 c    109 g     58 t
ORIGIN


  Query Match             2.7%;  Score 36;  DB 10;  Length 358;
  Best Local Similarity   58.3%;  Pred. No. 28;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||||| | |
Db     222 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 281

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     282 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 329


RESULT  34
AI392198/c
```

```
LOCUS       AI392198                384 bp    mRNA    linear   EST 03-FEB-1999
DEFINITION  NCSM1D6T3 Subtracted Mycelial Neurospora crassa cDNA clone SM1D6 5'
            similar to dolichyl-phosphate-mannose synthase, mRNA sequence.
ACCESSION   AI392198
VERSION     AI392198.1  GI:4220005
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
            Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
            Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R.
            , Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R.,
            Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig
            ,D.O.
  TITLE     Expressed sequences from conidial, mycelial, and sexual stages of
            Neurospora crassa
  JOURNAL   Fungal Genet. Biol. 21, 348-363 (1997)
  MEDLINE   97435549
COMMENT     Contact: Natvig,D.O./Nelson,M.A.
            Department of Biology
            University of New Mexico
            Castetter Hall, Albuquerque, NM 87131, USA
            Tel: 505 277 3411
            Fax: 505 277 0304
            Email: ngp@biology.unm.edu.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="Neurospora crassa"
                     /strain="74-OR23-IV A (FGSC 2489)"
                     /db_xref="taxon:5141"
                     /clone="SM1D6"
                     /clone_lib="Subtracted Mycelial"
                     /sex="Mating type A"
                     /tissue_type="Mycelium"
                     /dev_stage="Mycelium"
                     /lab_host="E. coli"
                     /note="Vector: pBlueScript SK (-); Site_1: EcoRI; Site_2:
                     XhoI; 2% sucrose for 24 hours.  cDNA directionally cloned
                     into pBluescript  SK(-) using the Uni-ZAP XR vector system
                     (Stratagene, La Jolla,  CA). Previously identified highly
                     expressed clones were subtracted  from this library."
BASE COUNT       90 a    140 c     70 g     73 t     11 others
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 384;
  Best Local Similarity   46.9%;  Pred. No. 29;
  Matches   99;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy    717 catcaattatcaagatgtaattgccatcggacgtttgtttgcaacaggccgtctgaacac 776
          | || || || | |||||| ||||| | ||     ||   ||       |       |   |
Db    378 CGTCCATGATGATGATGTAGTTGCCCTTGGCGAACTGGAGGCCGTGAACGTAGGCAGTGC 319

Qy    777 cgagcgcgtgattgctttgggtggttctcaagtcaacaaaccacgcctcttgcgtaccgt 836
          ||||  || | |||| |  |  |||   ||  |  ||       || |   || || ||
Db    318 CGAGTCCGAGCTTGCCTGNGCGGGTCTGCAGTTGCACGTGGGGAGCGTAGAGCTTAACGA 259

Qy    837 tttgggtgcgaaagtatcgcaaattactgcgggcgaattggttgacgcagacaaccgcgt 896
            |||| |   |  | | |         | ||| |   | || ||||   |  |   |
Db    258 GCTGGGCGGCGACATNTTGGGTGCCGTAGGGGGAGCNGTCGTNGACGATTANGAGTTCCC 199

Qy    897 gatttccggttcggtattgaacggcgcgatt 927
            |    | || | |    || || ||||||
Db    198 AGTCGANGTTTTGCTNGCTAAAGGTGCGATT 168


RESULT  35
AI306569
LOCUS       AI306569                393 bp    mRNA    linear   EST 09-DEC-1998
DEFINITION  qn23e08.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1899110 3'
            similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN. ;contains
            element MER22 repetitive element ;, mRNA sequence.
ACCESSION   AI306569
VERSION     AI306569.1  GI:3989640
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 353.
FEATURES             Location/Qualifiers
     source          1. .393
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1899110"
                     /clone_lib="NCI_CGAP_Lu5"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       85 a    127 c    116 g     65 t
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 393;
  Best Local Similarity   58.3%;  Pred. No. 29;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy    608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
          ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||| | |
Db    222 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 281

Qy    668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
          ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db    282 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 329


RESULT  36
AI609778
LOCUS       AI609778                400 bp    mRNA    linear   EST 12-MAY-1999
DEFINITION  tf83b11.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105853 3'
            similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN. ;contains
            element MER22 repetitive element ;, mRNA sequence.
ACCESSION   AI609778
VERSION     AI609778.1  GI:4618945
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 400)
```

```
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 372   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 387
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .400
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2105853"
                      /clone_lib="NCI_CGAP_Brn23"
                      /tissue_type="glioblastoma (pooled)"
                      /lab_host="DH10B"
                      /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of the modified pT7T3 vector.
                      Library is normalized, and was constructed by Bento
                      Soares and M.Fatima Bonaldo."
BASE COUNT       84 a    132 c    118 g     66 t
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 400;
  Best Local Similarity   58.3%;  Pred. No. 30;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||| | |
Db     222 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 281

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     282 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 329


RESULT  37
AA468664
LOCUS       AA468664                419 bp    mRNA    linear   EST 15-AUG-1997
DEFINITION  ne06c06.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880426 3'
            similar to SW:YEF1_YEAST P32622 HYPOTHETICAL 55.9 KD PROTEIN IN
            GDA1-UTR2 INTERGENIC REGION. ;contains element MER22 repetitive
            element ;, mRNA sequence.
ACCESSION   AA468664
VERSION     AA468664.1  GI:2195198
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
            , Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 778   Std Error: 0.00
            Seq primer: -41m13 fwd. ET from Amersham.
FEATURES              Location/Qualifiers
     source           1. .419
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:880426"
                      /clone_lib="NCI_CGAP_Co3"
                      /sex="pooled"
                      /tissue_type="colon"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was prepared from 12 pooled bulk tumor samples and primed
                      with a Not I - oligo(dT) primer. Double-stranded cDNA was
                      ligated to Eco RI adaptors (Pharmacia), digested with Not
                      I and cloned into the Not I and Eco RI sites of the
                      modified pT7T3 vector. Library went through one round of
                      normalization. "
BASE COUNT       89 a    138 c    121 g     70 t      1 others
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 419;
  Best Local Similarity   58.3%;  Pred. No. 30;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | ||||||| | |
Db     221 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 280

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     281 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 328


RESULT  38
AI300364
LOCUS       AI300364                477 bp    mRNA    linear   EST 01-FEB-1999
DEFINITION  qn22e08.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1899014 3'
            similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN. ;contains
            element MER22 repetitive element ;, mRNA sequence.
ACCESSION   AI300364
VERSION     AI300364.1  GI:3959710
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
```

```
           www-bio.llnl.gov/bbrp/image/image.html
           Insert Length: 807   Std Error: 0.00
           Seq primer: -40UP from Gibco
           High quality sequence stop: 370.
FEATURES             Location/Qualifiers
     source          1. .477
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1899014"
                     /clone_lib="NCI_CGAP_Lu5"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       98 a    152 c    135 g     91 t      1 others
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 477;
  Best Local Similarity   58.3%;  Pred. No. 32;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | |||||||| | |
Db     204 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 263

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     264 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 311


RESULT  39
AI039130
LOCUS       AI039130                486 bp    mRNA    linear   EST 28-AUG-1998
DEFINITION  ox31a04.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
            IMAGE:1657902 3' similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD
            PROTEIN. ;contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION   AI039130
VERSION     AI039130.1  GI:3278324
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1549   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 479.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1657902"
                     /clone_lib="Soares_total_fetus_Nb2HF8_9w"
                     /dev_stage="8-9 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from pooled 8-9 week
                     (total) fetus material with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAATTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       99 a    157 c    140 g     90 t
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 486;
  Best Local Similarity   58.3%;  Pred. No. 33;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | |||||||| | |
Db     217 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 276

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     277 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 324


RESULT  40
AI378387
LOCUS       AI378387                488 bp    mRNA    linear   EST 18-MAR-1999
DEFINITION  tc78e04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2070750
            3' similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN.
            ;contains element TAR1 repetitive element ;, mRNA sequence.
ACCESSION   AI378387
VERSION     AI378387.1  GI:4188240
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 793   Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2070750"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT       94 a    161 c    143 g     90 t
ORIGIN
```

```
  Query Match             2.7%;  Score 36;  DB 9;  Length 488;
  Best Local Similarity   58.3%;  Pred. No. 33;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy    608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
          ||||| ||  |  |    ||  ||  | |||   ||||    |||| |||||||| | |
Db    222 ATGCTACCCGCTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGGCTGGTTTGAGAGCCT 281

Qy    668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
          ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db    282 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 329


RESULT  41
AI701002
LOCUS       AI701002                497 bp    mRNA    linear   EST 18-DEC-1999
DEFINITION  we09e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340614 3'
            similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN C1B1.02C
            IN CHROMOSOME I. ;contains element MER22 MER22 repetitive element
            ;, mRNA sequence.
ACCESSION   AI701002
VERSION     AI701002.1  GI:4988902
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 497)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 760   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 461.
FEATURES             Location/Qualifiers
     source          1. .497
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2340614"
                     /clone_lib="NCI_CGAP_Lu24"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT       98 a    162 c    144 g     93 t
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 497;
  Best Local Similarity   58.3%;  Pred. No. 33;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy    608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
          ||||| || ||  |    ||  ||  | |||   ||||    || | |||||||| | |
Db    222 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 281

Qy    668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
          ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db    282 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 329


RESULT  42
AW006812
LOCUS       AW006812                526 bp    mRNA    linear   EST 10-SEP-1999
DEFINITION  wt07f12.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506799 3'
            similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD PROTEIN C1B1.02C
            IN CHROMOSOME I. ;contains element MER22 MER22 repetitive element
            ;, mRNA sequence.
ACCESSION   AW006812
VERSION     AW006812.1  GI:5855590
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
            , Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arraying: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 470.
FEATURES             Location/Qualifiers
     source          1. .526
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2506799"
                     /clone_lib="NCI_CGAP_Co3"
                     /sex="pooled"
                     /tissue_type="colon"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from 12 pooled bulk tumor samples and primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library went through one round of
                     normalization. "
BASE COUNT      106 a    165 c    143 g    111 t      1 others
ORIGIN


  Query Match             2.7%;  Score 36;  DB 9;  Length 526;
  Best Local Similarity   58.3%;  Pred. No. 34;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy    608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
          ||||| || ||  |    ||  ||  | |||   ||||    || | |||||||| | |
Db    204 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 263

Qy    668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
          ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db    264 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 311


RESULT  43
AI743812
```

```
LOCUS       AI743812                544 bp    mRNA    linear   EST 19-DEC-1999
DEFINITION  wg42b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:2367737 3' similar to TR:O13863 O13863 HYPOTHETICAL 60.7 KD
            PROTEIN C1B1.02C IN CHROMOSOME I. ;contains element MER22
            repetitive element ;, mRNA sequence.
ACCESSION   AI743812
VERSION     AI743812.1  GI:5112100
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 544)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1033   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 496.
FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2367737"
                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NbHSF pool 1:
                     309384-310919, 323208-325895 Soares Nb2HP pool 1:
                     145032-147335, 147720-148103, 148872-149255, 15002 -
                     150407, 151176-152327 Soares Nb2HF8-9W pool 1:
                     758280-760583, 772104-774407 Soares NbHPA pool 1:
                     304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                     pool 1:  723720-726407, 739080-740999 Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
BASE COUNT      106 a    173 c    154 g    111 t
ORIGIN
```

```
  Query Match             2.7%;  Score 36;  DB 9;  Length 544;
  Best Local Similarity   58.3%;  Pred. No. 34;
  Matches   63;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy     608 atgctgccaacatcgaaacacatgaattcggcggcccgcatccggccggtttgagtggca 667
           ||||| || ||  |    ||  ||  | |||   ||||    || | |||||||| | |
Db     222 ATGCTACCCACTCCCCTCCATCTGTGTGCGGGACCCCGTGAGCGACTGGTTTGAGAGCCT 281

Qy     668 cgcacattcatttcattgagccggtcggtgcaaacaaaaccgtttgga 715
           ||| || |   | |||||   ||  |||   || |||  ||  || ||
Db     282 CGCCCAGTGCCTGCATTGGAACGTCCGGAAGAAGCAAGCCCACTTCGA 329
```

```
RESULT  44
CNS0091P/c
LOCUS       CNS0091P                925 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL053013
VERSION     AL053013.1  GI:4934461
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .925
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR19D16"
                     /note="end : TET3"
BASE COUNT      120 a     61 c     61 g    172 t    511 others
ORIGIN
```

```
  Query Match             2.7%;  Score 36;  DB 12;  Length 925;
  Best Local Similarity   11.9%;  Pred. No. 44;
  Matches   34;  Conservative  128;  Mismatches  124;  Indels    0;  Gaps    0;

Qy     388 gcgctgcgtanccgtccgttcagcaaaatccctgccgtcgatgccgagccgttcgccatc 447
           :::: ::: :  ::  ::: :  :     ::  :::: ::  :: : :::: |:: |::|
Db     914 SSBSCSSSSMSTSSSNSSBCSSCSSSBSSSSTSSMSSSSBSSSSGSSSSSSGTSSACVKC 855

Qy     448 ttcgtcaatgcgatggacaccaatccgctngcggcagaccctgtggttgtgatcaaagaa 507
           :: |   |||: :  : ::   |||:    |: ::|:   |::|  : ||   : :
Db     854 NASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSGGASASHSSSS 795

Qy     508 gccgncgangatttcagacgangtntgctggtattgagccgtttgaccgagcgtaaaatc 567
           |:: ::  :|  ::|: ::  :   :  || |  :  :::   : :::|: | ::   :
Db     794 ACBSSSSSCSASCWSASSSSSASSSRSRSGGGAGGSGASSSRSSSSSSSASAGSVVSSAS 735

Qy     568 catgtgtgtaaggcagctggcgcagacgtgccgtctgaaaatgctgccaacatcgaaaca 627
           :  :   : :  ::: :  :|:: : :: : :: : :  |   : :||  :: |:   :|
Db     734 SSSSSCSSSVSCSSVASSMSCSSBSSSSASASSSSSSSSASCASCSCCCTSWSCSCSTSA 675

Qy     628 catgaattcggcggcccgcatccggccggtttgagtggcacgcaca 673
           ::  |:  ::::::|:::::  ::: :::   : : :|: ::: :|
Db     674 SMSAARSSSSSSSSCSSSSMSASSSASSSSASSSSSSGSSSSSGSA 629
```

```
RESULT  45
CNS01KFO/c
LOCUS       CNS01KFO                932 bp    DNA     linear   GSS 12-JUN-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 16023 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL148277
VERSION     AL148277.1  GI:7006423
KEYWORDS    GSS.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
```

```
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1  (bases 1 to 932)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 932)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .932
                     /organism="Anopheles gambiae"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="16O23"
                     /clone_lib="NotreDame1"
                     /note="end : T7"
BASE COUNT      159 a    278 c    269 g    215 t     11 others
ORIGIN


  Query Match             2.7%;  Score 35.8;  DB 12;  Length 932;
  Best Local Similarity   50.0%;  Pred. No. 51;
  Matches   82;  Conservative    1;  Mismatches   81;  Indels    0;  Gaps    0;

Qy      74 tcattaccgaagtcgcgttgcttggcgaagaatatgccggtatgcgccccctngatgaaag 133
           | || | |   | || |  | ||| ||  ||||||| |||   | |  |||   |  |||
Db     779 TGATGAACCTGGCCGAGAAGTTTGACGTGGAATATGACGGCTGGGGAACCTACTTCGAAG 720

Qy     134 tcaaggaaggcgatgccgtcaaaaaaggccaagtgctgtttgaagacaaaaagnatccgg 193
           | | || || | || | || ||||| | |       | | | | |  |  |     |
Db     719 ATCCGAACGGTGAAGACGGCGAAGAAGGCGACGACGAAGATTACGTCGACGAAGACGACG 660

Qy     194 gcgtggtgtttaccgcgccngtttcaggcaaaatcgccgccatc 237
           ||  |||  |  |    |  |||||||:        ||||| |
Db     659 ACGGCGTGCGTCACTAAGCGTTTTCAGGSGTGGCGCGCGCCACC 616


Search completed: June 29, 2002, 22:06:22
Job time: 17555 sec
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